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US-09-462-569B-4/c
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US-08-113-646A-44
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SEQ ID NO 4
LENGTH: 36
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Sequence 44, Appl
Sequence 19, Appl
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Sequence 4, Appli
Sequence 4, Appli
                                                                          2, 2004, 03:26:18; Search time 154 Seconds (without alignments) 7560.305 Million cell updates/sec
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Sequence 147:
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Sequence 1
Sequence 1
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.: /cgn2_ 6/ptodata/2/ina/5A_COMB.seq:*
.: /cgn2_ 6/ptodata/2/ina/5B_COMB.seq:*
.: /cgn2_ 6/ptodata/2/ina/6A_COMB.seq:*
.: /cgn2_ 6/ptodata/2/ina/6B_COMB.seq:*
.: /cgn2_ 6/ptodata/2/ina/6B_COMB.seq:*
.: /cgn2_ 6/ptodata/2/ina/ptoTUS_COMB.seq:*
.: /cgn2_ 6/ptodata/2/ina/ptoTUS_COMB.seq:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-113-646A-44
US-08-771-624B-1
US-08-44-209-4
US-08-439-996-4
US-08-439-996-4
US-09-420-443-1
US-09-621-976-14715
US-09-621-976-14715
US-09-621-976-14715
US-09-165-239A-5
US-08-984-916-3
US-08-83-123-3
US-09-08-123-7
US-09-268-505B-13
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US-09-738-274-35
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                                                                                                                                                                                                         682709 seqs, 277475446 residues
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                                                     using sw model
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Gapop_60.0 , Gapext 60.0
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Match Length DB
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2098
                                                     nucleic search,
                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 50
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                                                                                                                        Title:
Perfect score:
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                                                                                                                                                 Sequence:
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Sequence 4, Application US/09462569B
Patent No. 6392124
GERREAL INFORMATION:
APPLICANT: PONZ ASCASO, Fernando
APPLICANT: PONZ ASCASO, Fernando
APPLICANT: PONZ ASCASO, Fernando
APPLICANT: PANCHEZE, Florentina
APPLICANT: BANCHEZE, PROTENTINA
TITLE OF INVENTION: THE TURNIP WOSAIC VIRUS (TuMV)
TITLE OF INVENTION: THE TURNIP MOSAIC VIRUS (TuMV)
FILE REPERRACE: P/613-110
CURRENT FILING DATE: 2000-04-03
FRIOR APPLICATION NUMBER: DCT/5S98/00200
PRIOR APPLICATION NUMBER: ES P 9701522
FRIOR PILING DATE: 1998-07-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTI VOF: 2.0
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100.0%; Pred. No. 0.0002;
iive 0; Mismatches 0; Indels
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Patent No. 557846B
GENERAL INFORMATION:
APPLICANT: PICKUP, David J.
APPLICANT: PATEL, Dhavalkumar
TITLE OF INVENTION: SITE-SPECIFIC RNA CLEAVAGE
TITLE OF INVENTION: SITE-SPECIFIC RNA CLEAVAGE
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
US-08-233-609-5
US-08-381-572-20
US-08-286-304-5
US-08-442-745-5
US-08-443-1129-5
US-08-443-1130-5
US-08-443-130-5
US-08-88-911-5
PCT-US95-04467-5
US-09-244-794A-11
US-09-244-794A-12
US-09-244-794A-13
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ORGANISM: Artificial Sequence
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Matches 32; Conservative
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Gaps

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SEE: Behring Diagnostics GmbH, c/o Dade Behring Inc.: 1717 Deerfield Road
Deerfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Homogeneous Amplification and Detection IIITLE OF INVENTION: of Nucleic Acids
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STATE: 1111018

ZIP: 60015-0778

ZIP: 60015-0778

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/771,624B

FILING APPLICATION TATA:
PILING APPLICATION BTA:
APPLICATION NUMBER: US 60/009,090
FILING APPLICATION TATA:
APPLICATION NUMBER: 12.DEC-1995
CLASSIFICATION TORDER: 35.074

REGISTRATION NUMBER: 39.074

REFERENCE/DOCKET NUMBER: 1030
TELEPHONE: (847) 267-5364

TELEFAX: (847) 267-5364

TELEFAX: (847) 267-5024

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
1.5%; Score 32; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 32; Conservative 0; Mismatches 0;
Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 32; Conservative 0; Mismatches 0;
                                                                                    2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
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                                                                                                                                            38 далалалалалалалалалалалалалалалал 7
                                                                                                                                                                                                                                                                             Sequence 1. Application US/08771624B
Patent No. 5914230
GENERAL INFORMATION:
APPLICANT: Liu, Yen Ping
APPLICANT: Rurn, Nurith
APPLICANT: Kurn, Nurith
APPLICANT: Lin, Claire
APPLICANT: Lin, Claire
APPLICANT: Ulman, Edwin F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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US-08-771-624B-1/c
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STREET: 17
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US-08-440-209-4/c
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Sequence 19, Application US/09720201A

Patent No. 6524853

GENERAL INFORMATION:
APPLICANT: KOHARA, MICHINORI
APPLICANT: KOHARA, MICHINORI
APPLICANT: TAIRA, KAZUNARI
APPLICANT: OHNORI, HIROSHI
TITLE OF INVENTION: AUCTOR EXPRESSING AN VIRAL FULL-LENGTH GENE AND
TITLE OF INVENTION: A UCTOR EXPRESSING AN VIRAL FULL-LENGTH GENE AND
TITLE OF INVENTION: A UCTOR EXPRESSING AN VIRAL FULL-LENGTH GENE AND
TITLE OF INVENTION: A US/09/720,201A
TITLE OF INVENTION: A UNMERR: US/09/720,201A
FILE OF INVENTION UNMERR: US/09/720,201A
CURRENT FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: P 98/177,820
PRIOR APPLICATION NUMBER: P 98/177,820
PRIOR PELING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 25
SOFTWARE PATENT VET. 21
SEQ ID NO 19
LENGTH: 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
1.5%; Score 32; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 32; Conservative 0; Mismatches 0; Indels
                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/113,646A
FILING DATE: 31-AUG-1993
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 07/084,406
PILING DATE: 10-AUG-1987
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARX J.
REGISTRATION NUMBER: 32,955
REGISTRATION NUMBER: 1579-20
TELEFAM: (703) 816-4100
TELEFAM: (703) 816-4100
TELEFAM: (703) NINVORMATION:
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        1100 NORTH GLEBE ROAD
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MOLECULE TYPE: RNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                VIRGINIA
                                                                                       COUNTRY: U.S.A.
                                   ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-720-201A-19/c
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; Sequence 4, Application US/08440209

DB 4; Length 38;

1.5%; Score 32;

Query Match

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Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                        MEDIUM TYPE:
                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
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US-09-732-067-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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; Patent No. 592285,
; GENERAL INFORMATION:
; APPLICANT: Han, Jang H
; APPLICANT: Spacete, Richard R
; TITLE OF INVENTION: Translation of HCV Proteins
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield, and Sacks P.C.
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·.
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APPLICANT: Han, Jang H
APPLICANT: Han, Jang H
APPLICANT: Methods and Compositions for Controlling
TITLE OF INVENTION: Translation of HCV Proteins
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield, and Sacks P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 40;
                                                                                                                                                                                                                                                                               COMPUTER RELACE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,209
FILING DATE: 12-MAY-1995
CLASSIFICATION: 0A74:
APPLICATION NUMBER: 08/477,895
FILING DATE: 06-JUN-1995
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US/08/128,583
FILING DATE: 28-SEP-1993
ATTONENEY/AGENTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.5%; Score 32; DB 2; Le Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 32; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Janiuk, Anthony J
REGISTRATION NUMBER: 29,809
REFERENCE/DOCKET NUMBER: C0772/7004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFRAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08439996
Patent No. 6057093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02210
COMPUTER READABLE FORM:
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CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 02210
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US-08-439-996-4/c
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COMPATING SYSTEM: FOR PC-DOG/NS-DOS
OFFERENTIAG SYSTEM: FOR PC-DOG/NS-DOS
OFFERENTIAG PARENTIA Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/439.996
FILING DARIE 1881: US/08/477.895A
FILING DARIE 18-89193
ATTORNEY/AGRIT INFORMATION:
APPLICATION NUMBER: US/08/477.895A
FILING DARIE 18-89199
ATTORNEY/AGRIT INFORMATION:
APPLICATION NUMBER: US/08/477.895A
FILING DARIE 18-89199
ATTORNEY/AGRIT INFORMATION:
TELECHOMER: 617-720-240
TELECHOMER: 617-720-240
TELECHOMER: 617-720-241
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TELECHOMER: 617-720-340
TELECHOMER: 617-730
TELECHOMER: 617
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1.5%; Score 32; DB 4; Length 50;
100.0%; Pred. No. 0.0002;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                    US-09-61-976-14715
US-09-621-976-14715
US-09-621-976-14715
Sequence 14715, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPRENCE: GENSET.054PR.2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SEQ ID NO 14715
FILE REPRENCE: FALCH DUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32; DB 4; Ler
Pred. No. 0.0002;
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100.0%; Pred. No. 0.00055;
tive 0; Mismatches 0;
                                                                                         2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
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GENERAL INFORMATION:
TILLE OF INVENTION: A Transcription Factor TITLE OF INVENTION: A Transcription Factor; FILE REFERENCE: 4464.204-US; CURRENT FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: 0740/96
EARLIER APPLICATION NUMBER: 0740/96
EARLIER PILING DATE: 1996-07-05
EARLIER FILING DATE: 1996-07-05
EARLIER FILING DATE: 1997-07-07
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 9
IENGTH: 41
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31; Conservative
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                                                 32; Conservative
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COTHER INFORMATION: Primer
US-09-197-814-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity
      Query Match
Best Local Similarity
Matches 32; Conserv
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US-09-197-814-9/c
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Patent No. 663963
FABERAL INFORMATION:
APPLICANT: Undert, S.
APPLICANT: Glockano, J.Y.
TITLE OF INVENTYON: ESTS and Encoded Human Proteins.
FILE REPERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 14612
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CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION NUMBER: US/08/420,443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 05663/002001
TELECOMMULICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                              NUCLEIC ACID PROBES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASCIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/990,298
FILING DATE: 1921210
ATTORNEY/AGENT INFORMATION:
NAME: Y. ROCKY TSAO
REGISTRATION NUMBER: 34,053
                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: C. Bruce Bagwell
TITLE OF INVENTION: NUCLEIC ACID
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
SURESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                 US-08-420-443-1
; Sequence 1, Application US/08420443
; Patent No. 5607834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 32; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: sing
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RESULT 12 US-09-920-581-9/c

, ORGANISM: Homo sapiens US-09-621-976-14612

TYPE: DNA

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Sequence 3, Application US/09894916
Patent No. 6642361
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hunter, Fina F.
APPLICANT: Bidochka, Michael J.
TITLE OF INVENTION: Encoding Such Protein From Simulium Vittatum And Nucleic ACTIVE OF INVENTION: Encoding Such Protein
FILE REPERENCE: 1468-001A
CURRENT APPLICATION NUMBER: US/09/894,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                     APPLICANT: Evans, Cheryl
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Bowman, Michael
TITLE OF INVENTION: ENCERTED PROTEINS AND POLYNUCLECTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.5%; Score 31; DB 1; Length 44;
100.0%; Pred. No. 0.00055;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     SPETWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/664,596B
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PRIOR FILING DATE: 2000-06-29
NUMBER: Patentin version 3.1
SEQ ID NO 3
LENGTH: 45
TYPE: DNA
ORGANISM: Simulium vittatum
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BYOWN, SCOLT A.
REGISTRATION NUMBER: 32,724
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 476-5851
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
         Treacy, Maurice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                             Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature LOCATION: (44)...(45)
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Best Local Similarity
Matches 31; Conserva'
                                                                                                                                                                                                                                CITY: Cambridge
STATE: Massachus
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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APPLICANT: JOHNSON, ALEXANDER
APPLICANT: JOHNSON, ALEXANDER
APPLICANT: BRAUN: BUCKNUCLECTIDE SEQUENCES FROM CANDIDA
TITLE OF INVENTION: POLYNUCLECTIDE SEQUENCES FROM CANDIDA
TITLE OF INVENTION: GROWTH
TITLE OF INVENTION: GROWTH
FILE REFERENCE: 220022000700
CURRENT APPLICATION NUMBER: US/09/165,239A
CURRENT APPLICATION NUMBER: 60/068,065
PRIOR FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 13-18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5.
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100.0%; Pred. No. 0.00055;
tive 0; Mismatches 0;
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                                                         APPLICANT: Christensen, Tove
TITLE OF INVENTION: A Transcription Factor
TITLE OF INVENTION: A Transcription Factor
CURRENT APPLICATION NUMBER: US/09/920,581
CURRENT FILING DATE: 2001-08-01
PRIOR PRICATION NUMBER: 09/197,814
PRIOR FILING DATE: 1998-11-23
PRIOR FILING DATE: 1998-11-23
PRIOR FILING DATE: 1997-07-07
NUMBER OF EQ ID NOS: 14
SOFTWARE: FASTERQ for Mindows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 AAAAAAAAAAAAAAAAAAAAAAAAAA 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 9, Application US/08664596B
; Patent No. 5807703
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: LaVallie, Edward
; APPLICANT: Racie, Lisa
; APPLICANT: Recie, Lisa
; APPLICANT: Merberg, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 5, Application US/09165239A
; Patent No. 6344554
Sequence 9, Application US/09920581
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LaVallie, Edward
Racie, Lisa
Merberg, David
                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.(
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Primer
                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-165-239A-5/c
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                                                                                                                                                                                                                                                                                                                    SEQ ID NO 9
LENGTH: 41
                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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RESULT 14

0;

0; Gaps Query Match 1.5%; Score 31; DB 4; Length 45; Best Local Similarity 100.0%; Pred. No. 0.00055; Matches 31; Conservative 0; Mismatches 0; Indels

0

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Search completed: July 2, 2004, 07:38:41 Job time: 158 secs

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Sequence 4651, App
Sequence 14, Appl
Sequence 18, Appl
Sequence 21, Appl
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Sequence 10175, A
Sequence 6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Appl
Sequence 21, Appl
Sequence 2, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 22, Appli
                                                                                                                                                          (without alignments)
5530.704 Million cell updates/sec
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                                                                                                                                                                                                                                                                            Sequence 26, P
Sequence 2, P
Sequence 9, P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications NA:*

| cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: / cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: / cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
4: / cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5: / cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
6: / cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
7: / cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
8: / cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
9: / cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
10: / cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
11: / cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
12: / cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
13: / cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
14: / cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
15: / cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
16: / cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
16: / cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
16: / cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
17: / cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
18: / cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
19: / cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
                                                                                                                                     2, 2004, 03:36:20 ; Search time 1830 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-827-289-14
US-09-827-289-18
US-09-827-289-21
US-09-827-289-21
US-09-827-289-22
US-09-828-034-2
US-09-827-289-22
US-09-827-289-22
US-09-827-289-26
US-09-827-289-26
US-09-827-289-26
US-10-371-600-9
5 US-10-371-600-9
5 US-09-764-891-10175
5 US-09-764-891-10175
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                                                                                                                                                                                                                                                                                                                                                                                         3163042 seqs, 2412103800 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                       OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                     OLIGO_NUC
Gapop_60.0 , Gapext 60.0
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Match Length DB
                                                                                                                                                                                                                            US-09-445-223-2
2098
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                                                                                                                                     July
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                                                                                                                                                                                                                                                 Perfect score:
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                                                                                                                                                                                                                            Title:
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2.5 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0	Sequence 28, Appl Sequence 29, Appl
-10 - 463 - 549 - 2 -10 - 218 - 567 - 7 -10 - 218 - 567 - 7 -10 - 289 - 921 - 5 -10 - 668 - 148 - 1 -10 - 668 - 148 - 1 -10 - 681 - 343 - 10 -10 - 681 - 343 - 10 -10 - 971 - 105 - 1 -10 - 107 - 105 - 1 -10 - 114 - 432 - 4 -10 - 314 - 578 - 1 -10 - 042 - 193A - 1 -10 - 042 - 193A - 1 -10 - 114 - 578 - 1 -10 - 042 - 193A - 1 -10 - 10 - 310 - 380 - 384 - 1 -10 - 10 - 30 - 386 - 1 -10 - 10 - 30 - 386 - 1 -10 - 10 - 30 - 386 - 1 -10 - 310 - 310 - 1 -10 - 310 - 300 - 386 - 1 -10 - 310 - 310 - 300 - 386 - 1 -10 - 310 - 310 - 300 - 386 - 1 -10 - 310 - 310 - 300 - 386 - 1 -10 - 310 - 300 - 386 - 1	US-10-219-195-28 US-10-219-195-29
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ALIGNMENTS

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Sequence 4651, Application US/10131827

Sequence 4651, Application US/10131827

Publication No. US20040009479A1

Sequence 4651, Application Sequence 4651, Application No. US20040009479A1

APPLICANT: Worldgemuth, Jay

APPLICANT: FTY, Kirk

APPLICANT: Wordward, Robert

APPLICANT: Ly, NGOG

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE

FILLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE

FILLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE

FILLE OF INVENTION: 10/10131, 827

CURRENT APPLICATION NUMBER: US 10/006, 290

PRIOR APPLICATION NUMBER: US 60/296, 764

PRIOR FILING DATE: 2001-10-22

PRIOR FILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 9090

SEGFWARE: Patentin version 3.1
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2.4%; Score 50; DB 16; I
Best Local Similarity 100.0%; Pred. No. 4.3e-14;
Matches 50; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-827-4651
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RESULT 2 US-09-827-289-14/c ö

Gaps

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FEATURE:

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Length 46; Indels

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Sequence 25, Application US/09827289;
Sequence 25, Application US/09827289;
Parent No. US2002009716A1
GENERAL INFORMATION:
APPLICANT: Abarzua, Patricio
TITLE OF INVENTION: Extension
TITLE OF INVENTION: Extension
FILE REPERENCE: 469290-55;
CURRENT APPLICATION UNMER: US/09/827,289
CURRENT APPLICATION UNMER: US. 60/194843;
PRIOR PILING DATE: 2000-04-05;
NUMBER OF SEQ ID NOS: 35;
SOGTWARE: Patentin Ver. 2.1
; SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: P1 primer for ; OTHER INFORMATION: use in allele discrimination US-09-827-289-25
                                                                                                                                                                                                                                                                    ; FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
; OTHER INFORMATION: use in allele discrimination
US-09-827-289-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.6%; Score 34; DB 9; Length 46; Best Local Similarity 100.0%; Pred. No. 4.3e-06; Matches 34; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       1.6%; Score 34; DB 9; Li
100.0%; Pred. No. 4.3e-06;
tive 0; Mismatches 0;
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APPLICANT: Zhong, Zhi
APPLICANT: Hong, Zhi
APPLICANT: Ferrari, Eric
TITLE OF INVENTION: HOW REPLICASE COMPLEXES
FILE REFERENCE: IN01165
CURRENT APPLICATION NUMBER: US/09/828,034
CURRENT FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 33
CURRENT APPLICATION NUMBER: US/09/827,289 CURRENT FILING DATE: 2001-04-05 PRIOR APPLICATION NUMBER: U.S. 60/194843 PRIOR FILING DATE: 2000-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09828034 Patent No. US20020064771A1 GENERAL INFORMATION:
                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 34; Conservative
                                                                                                        NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver.
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US-09-827-289-25/c
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                                                                                                                                                              SEQ ID NO 21
LENGTH: 46
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Sequence 18, Application US/09827289;
Patent No. US20020009716A1;
GENERAL INFORMATION:
APPLICANT: Abarzua, Patricio
TITLE OF INVENTION: Extension
TITLE OF INVENTION: Extension
TITLE OF INVENTION: Extension
FILE REPERENCE: 469290-55
CURRENT APPLICATION NUMBER: US/09/827,289
CURRENT FILING DATE: 2001-04-05
PRIOR FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 35
NUMBER OF SEQ ID NOS: 35
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Sequence 14, Application US/09827289;
Patent No. US2002000971641
; GENERAL INFORMATION:
APPLICANTION:
TITLE OF INVENTION: Process for Allele Discrimination Using Primer
TITLE OF INVENTION: Extension
FILE REFERENCE: 469290-55
CURRENT APPLICATION NUMBER: US/09/827,289
CURRENT APPLICATION NUMBER: US. 60/194843
PRIOR APPLICATION NUMBER: U.S. 60/194843
PRIOR APPLICATION NUMBER: U.S. 60/194843
PRIOR APPLICATION NUMBER: U.S. 2001-04-05
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: OTHER INFORMATION: Description of Artificial Sequence: P1 primer for OTHER INFORMATION: use in allele discrimination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTHER INFORMATION: Description of Artificial Sequence: Pl primer for CTHER INFORMATION: use in allele discrimination
US-09-827-289-14
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Patent No. US2002009716A1

GENERAL INFORMATION:
APPLICANT: ADarzua, Patricio
TITLE OF INVENTION: Process for Allele Discrimination Using Primer
TITLE OF INVENTION: Excension
FILE REFERENCE: 469290-55
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1.6%; Score 34; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 34; Conservative 0; Mismatches 0;
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1.6%; Score 34; DB 9; L
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 34; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.1

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Query Match
Best Local Similarity 100.C
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US-10-371-600-2/c
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Fatent No. US20020009716A1;
GENERAL INFORMATION:
TITLE OF INVENTION: Process for Allele Discrimination Using Primer;
TITLE OF INVENTION: Extension;
FILE REPRENCE: 469290-55;
CURRENT APPLICATION NUMBER: US/09/827,289;
CURRENT FILING DATE: 2001-04-05;
FRIOR APPLICATION NUMBER: U.S. 60/194843;
FRIOR PILING DATE: 2000-04-05;
NUMBER OF SEQ ID NOS: 35;
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                         Gaps
                                                                                     ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-3
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US-09-827-289-22
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1.6%; Score 33; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 33; Conservative 0; Mismatches 0;
                                                                                                                                                                          1.6%; Score 33; DB 9; L
100.0%; Pred. No. 1.3e-05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                             2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
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                                                                                                                                                                                                                                                                                                                                             RESULT 7
US-09-828-034-3
i Sequence 3, Application US/09828034
j Patent No. US20020064771A1
i GENERAL INFORMATION:
i APPLICANT: Abong, Weidong
APPLICANT: Hong, Zhi
i APPLICANT: FILD ENTER IN Eric
TITLE OF INVENTION: HCV REPLICASE COMPLEXES
FILE REFERENCE: IN01165
i CURRENT APPLICATION NUMBER: US/09/828,034
CURRENT FILING DATE: 2001-04-06
i REIOR APPLICATION NUMBER: U.S. 60/195,852
PRIOR FILING DATE: 2000-04-06
i NUMBER OF SEQ ID NOS: 33
i SOFTWARE: PatentIn Ver. 2.1
i SEQ ID NO 3
i LENDTH: 36
i TENDTH: 36
i TENDTH: 36
                                                                                                                                                                                                                                                                                                     2 GAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34
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                                                              ORGANISM: Artificial Sequence
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                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 33; Conservative
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SEQ ID NO 2
LENGTH: 36
TYPE: RNA
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OTHER INFORMATION: Description of Artificial Sequence: Pl primer for
OTHER INFORMATION: use in allele discrimination
US-09-827-289-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 # Sequence 2, Application US/10371600
# Publication No. US20030180776A1
# GENERAL INFORMATION
# APPLICANT: WU, MING
# APPLICANT: WU, MING
# TITLE OF INVENTION DETECTION BY SLIDING TEMPLATE AMPLIFICATION
# FILE REPERENCE: 3817.10-2
# CURRENT PILING DATE: 2003-05-19
# PRIOR PAPLICATION NUMBER: 60/359,223
# PRIOR PAPLICATION NUMBER: 60/359,223
# PRIOR PPLICATION NUMBER: 60/359,223
# PRIOR PILING DATE: 2002-02-05
# PRIOR PILING DATE: 2002-05-08
# NUMBER OF SEQ ID NOS: 14
# SOFTWARE: PATENTIN VET: 2.1
# SOFTWARE: PATENTIN VET: 2.1
# SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Abarrau, Patricio
TITLE OF INVENTION: Process for Allele Discrimination Using Primer
TITLE OF INVENTION: Extension
TITLE OF INVENTION: Extension
FILE REFERENCE: 469290-55
CURRENT APPLICATION NUMBER: US/09/827,289
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: U.S. 60/194843
PRIOR PILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 26
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1.6%; Score 33; DB 9; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 33; Conservative 0; Mismatches 0; Indels
                                                                      Indels
                Score 33; DB 9; Le
Pred. No. 1.4e-05;
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1.6%; Scc. No. 1.
100.0%; Pred. No. 1.
0; Mismatches
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Patent No. US20020009716A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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TYPE: DNA ORGANISM: Homo sapiens
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LENGTH: 39
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; Publication No. US20030180776A1
; Remembal INFORMATION:
; APPLICANT: WU, MING
; APPLICANT: WU, MING
; FILE REPRENCE: 3817.10-2
; CURRENT APPLICATION NUMBER: US/10/371,600
; CURRENT APPLICATION NUMBER: 06/359,223
; FRICE REPRENCE: 2002-05-19
; PRIOR FILING DATE: 2002-05-6
; PRIOR APPLICATION NUMBER: 60/359,360
; PRIOR FILING DATE: 2002-05-08
; RUGHER REPRENCE: 1002-05-08
; PRIOR FILING DATE: 2002-05-08
; RUGHER PRIOR DATE: 2002-05-08
; RUGHER OF FILING DATE: 2002-05-08
; RUGHER OF FILING DATE: 2002-05-08
; RUGHER OF FILING DATE: 2002-05-08
; RUGHER OF SEQ ID NOS: 14
; SEQ ID NO 10
                                                                                                                                                                                                                    APPLICANT: WU, MING
APPLICANT: WU, MING
APPLICANT: WU, MING
TITLE OF INVENTION: DETECTION BY SLIDING TEMPLATE AMPLIFICATION
FILE REFERENCE: 3817.10-2
CURRENT APPLICATION NUMBER: US/10/371,600
CURRENT FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: 60/359,223
PRIOR APPLICATION NUMBER: 60/359,223
PRIOR APPLICATION NUMBER: 60/379,360
PRIOR APPLICATION NUMBER: 2002-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 9
LEMOTH: 32
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US-10-371-600-10
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llarity 100.0%; Pred. No. 4.2
Conservative 0; Mismatches
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                                                                                                                                                          Sequence 9, Application US/10371600 Publication No. US20030180776A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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US-10-371-600-10/c
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APPLICANT: Nakamura, Kumi
TITLE OF INVENTION: Probe Immobilized Substrate and Method for Manufacturing the Same
TITLE OF INVENTION: Analytical Method
FILE REPERENCE: 03560.003309
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; Publication No. US20030113337A1
; GENERAL INFORMATION:
   APPLICANT: MENUELO, Daniel
; APPLICANT: LEVIN, Brandi A.
; TITLE OF INVENTION: HIGH EFFICIENCY TISSUE SPECIFIC COMPOUND
; TITLE OF INVENTION: DELIVERY SYSTEM USING STREPTAVIDIN-PROTEIN A FUSION PROTEIN
; FILE REFERENCE: 5986/11123-US1
; CURRENT APPLICATION NUMBER: US/10/289,921
; CURRENT FILING DATE: 2003-02-27
; PRIOR FILING DATE: 1995-11-30
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                                                                             APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10175
LENGTH: 38
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SOFTWARE: FastSEQ for Windows Version 3.0
Sequence 10175, Application US/09764891; Publication No. US20030077808A1; GENERAL INFORMATION:
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Search completed: July 2, 2004, 08:09:22 Job time : 1834 secs

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CF332441 BU4311798 BU4311799 CF327755 CF302212 CF305212 CF305473 CF334384 BF582680 BX561724 CF332152 CF332152 CF33115383 AA852759 AI316598

A1037510 Homo sapi CF002212 7LEAF-07 CF003423 CLD-01-CF334384 JMT-01-CF334284 JMT-03-K BE561724 BX561724 CF332152 NACL-08-CF337040 JMT-07-F CF33393 JMT-07-F CF33393 JMT-03-B AA61723 VJ79605.X AA61723 VJ79605.X AA61723 VJ79605.X AA61723 VJ79605.X AN21575 WHTBCae03 AA61723 VJ79605.X AN21575 WHTBCae03 AA61723 VJ79605.X CR35626 NISC 1001 AN35626 NISC 1001 AN35626 NISC 1001 CF309345 ABF-03-F CF309345 ABF-03-F CF309345 ABF-03-F CF31171 HD-01-01-07-CF31171 NACL-03-CF31171 NACL-03-CF321046 HD-12-C1 CF321046 HD-12-C1 CF321040 HD-12-C1 CF321040 HD-12-C1 CF321040 HD-12-C1 CF321040 HD-12-C1

AZ587341 AA853120 AA617223

BI496942 BX558006 BX699285

AW215755

CA335626 AW327277 CF291773 CF299386 CF309233 CF309345

CF321046 CF328471 CF331270 AZ459536 AZ470832 AZ611890

AZ778018 DR85L21T

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AU106827 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
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Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
A-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
                                                                                                                                                                                                                                                                                                                                              HEP20988, mRNA sequence
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Homo sapiens (human)
Homo sapiens
11375929
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RESULT 1
AU106827
LOCUS
DEFINITION
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MEDLINE
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COMMENT
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AUTHORS
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KEYWORDS
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                                                                                    Description
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   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                      27513289 seqs, 14931090276 residues
                                                                                                                                                 parameters:
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                                                                                                                                                                                  summaries
                              nucleic search, using sw model
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AU106825
AU106826
AA564185
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Gapop_60.0 , Gapext 60.0
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em_gss_vrl:*
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em_gss_pro:*
em_gss_rod:*
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em_gss_inv:*
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em_gss_vrt: *
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ALIGNMENTS

CF311229 CF326967

CF291613

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Mammalia; Eutheria; Primates; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Sata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol type="mRNA"
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/db_caref="taxon:970"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GICTCTAGAAAAGAAGTCAGCTCTGGTTCGGAGAAGCAGC 50
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100.0%; Pred. No. 0;
iive 0; Mismatches
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CAS03470, mRNA sequence.
               AU106826
AU106826.1 GI:13556347
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AA564185/c
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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Sugano, S. Construction and characterization of a full length-enriched and a S'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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1. (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
                                                                                                                                                                                                                                                                                                                                                                50 bp mRNA linear EST 30-AUG-201
41068255 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
AU106825
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/mol_type="mRNA"
/db_raref="taxon:9606"
/clone="CASO1421"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                 Length 50;
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100.0%; Pred. No. v,
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larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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/organism="Homo sapiens"
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Gaps . 0

Length 50 0; Indels

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

EDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 203 Std Error: 0.00
AA564185 50 bp mRNA linear EST 04-SEP-1997
nj04d11.s1 NCI_CGAP_Pr21 Homo sapiens cDNA clone IMAGE:985365 3',
                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 50)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
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Seg primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                           AA564185.1 GI:2335824
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AU106826 5ugano Homo sapiens cDNA library Homo sapiens cDNA clone

DEFINITION

LOCUS

RESULT 3 AU106826

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2063 ТІТСАРАРАРАРАРАРАРАРАРАРАРАРАРАРА 2096
                                                                                                                                                                                                                                                                   BU431798.1 GI:22770280
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BU431799/c
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AUTHORS
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                                                                                                                                                                                /idone lib="NOT CGAP Pr21"
//lone lib="NOT CGAP Pr21"
//lone lib="NOT CGAP Pr21"
//loce="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Ist strand cDNA was prepared
from normal prostate bulk tissue, and was then primed with
a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is not normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo. "
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40 bp mRNA linear EST 18-AUG-2003
NACL--08-P05.bl Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--08-P05, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enthartoideae; Oryzeae; Oryza.

1. (bases 1 to 40)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.T., Kim,J.K., Kim,Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University Yongjin, Kyeongqi, Korea Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and Then used as templates for RT-PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                1.7%; Score 35; DB 9; Length 50;
100.0%; Pred. No. 0;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2064 TTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 TTGAAAAAAAAAAAAAAAAAAAAAAAAAAA 10
                                                                                                                                                 /tissue_type="normal prostate"
/lab_host="DH10B"
                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
                                                                                                         clone="IMAGE:985365"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="NACL--08-P05"
Location/Qualifiers
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                                                                                                                             /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35; Conservative
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Best Local Similarity
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BU431798 33 bp mRNA linear EST 09-SEP-2002
601655890R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855694 3',
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/tab host="PHIOB (phage-resistant)"
/clone_lib="NIH MGC_6"
/note="Corgan: ovary; Vector: pCMV-SPORT6; Site_1: NotI;
/notice="Corgan: ovary; Vector: pCMMV-SPORT6; Site_1: NotI;
/notice="Corgan: ovary; Vector: pCMMV-SPORT6; Site_1: NotI;
/notice="Corgan: ovary; Vector: pCMMV-SPORT6; Site_1: NotI
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NIH-MGC http://mgc.nci.nih.gov/.
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1 (bases 1 to 34)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM570 row: c column: 23
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33 СААДАДАДАДАДАДАДАДАДАДАДАДАДАДАД
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Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:3855694"
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Location/Qualifiers
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Unpublished (1999)

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Eukaryoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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7LEAF--07-114.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-114, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="DKFZp564E1872"
/clone llb="564 (synonym: hfbr2). Vector pAMP1; host
X1-2blue; sites NotI + SalI"
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Please contect the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases. MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
                                         Length 39;
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59, Last updated, Version 1)
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                                      1.6%; bccd. No. v,
100.0%; Pred. No. v,
... 0; Mismatches
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100.0%; Pred. No. 0;
tive 0; Mismatches
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/db xref="taxon:9606"
/mol_type="mRNA"
/organism="Homo_sapiens"
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens mRNA; EST DKFZp564E1872_rl
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                                                                                                                                                                                                                               standard; mRNA; EST; 40
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                                                                                                                                                                                                                                                                                                                                                                                                                  EST; expressed sequence tag.
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Best Local Similarity 100.
Matches 33; Conservative
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                                                                                 33; Conservative
RT-PCR."
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                                                            Best Local Similarity
Matches 33; Conserv
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12-MAR-1999 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enhartoidaes; Oryzeae; Oryza.

1 (Dases 1 to 39)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
                                                                                                                                                                                                                                 Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University Yroqin, Kyongqi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355
 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
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100.0%; Pred. No. v,
... 0; Mismatches
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    .39
    /organism="Oryza sativa"

                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                        High quality sequence stop: 31.
Location/Qualifiers
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/clone="NACL--02-F23"
/tissue_type="callus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/cultivar="Nackdong"
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KEYWORDS

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VERSION

JOURNAL COMMENT

TITLE

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Eukaryota; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enhartoideae; Oryza.

E. 1. (bases 1 to 44)

Song,S.1., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yonglin, KyeongJi, Korea
Tel: 82 31 330 6193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CF334384

44 bp mRNA linear EST 18-AUG-2003
JMT--03-K14.bl AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--03-K14, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="leaf"
/dev stage="14 days after germination"
/dev stage="14 days after formination"
/dev stage="14 days after formination"
/dev stage="14 days"
/dev stage="14 days
                                                                                                                                                                                                /tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice cold treated leaf plasmid cDNA library
(CLO)F
                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. Oligo-capped nRNA was reverse transcribed and then used for PCR."
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100.0%; Pred. No. 0;
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    Location/Qualifiers
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                                                                                                            /db_xref="taxon:4530"
/clone="CLD1--01-M22"
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                       /mol_type="mRNA"
/cultivar="Nackdong"
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                                                                                                                                                                              Oryza sativa

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzae, Oryzae,
1 (bases 1 to 44)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Uniquation (2007)
Contact: Nahm B.H.
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yogin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Eax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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100.0%; Pred. No. 0;
cive 0; Mismatches 0; Indels
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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CF302212
CF302212.1 GI:33673973
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LOCUS

ACCESSION

ORGANISM

KEYWORDS SOURCE

TITLE JOURNAL

COMMENT

REFERENCE AUTHORS

CF305473/c

RESULT 11

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VERSION KEYWORDS

ORGANISM

AUTHORS TITLE JOURNAL COMMENT

FEATURES

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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Dryzaa.

El Chaees I to 46)

S Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.T., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTS

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A6 bp mRNA linear BST 18-AUG-2003 sativa cDNA clone NACL--08-120.gl Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--08-120, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="country: Zimbabwe; EST from adult gut infected with T.brucei"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
                                      Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 15A, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Eehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the CDNA all plc reads are from
the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db xref="taxon:37546"
/clone="Tse57d10 glc"
/tissue type="adult infected gut"
/clone_lib="Glossina morsitans adult infected
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    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                     1. .46
/organism="Glossina morsitans morsitans"
/mol type="mRNA"
/sub_species="morsitans"
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/clone="NACL--08-120"
/tissue_type="callus"
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/cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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| coganism="Mus musculus" |
| nol_type="mRN4" |
| strain="mRN4" |
| db_xref="taxon:10090" |
| db_xref="taxon:10090" |
| db_one="InMags:420837" |
| lab_host="DHIOB (T1 phage-resistant)" |
| clone lib="NCI CGAP_Co24" |
| note="Organ: colon; Vector: pCMV-SPORT6; Site_I: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Site_b: site_1: kb. Constructed by Life |
| Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BX561724 Glossina morsitans morsitans adult infected gut Glossina morsitans clone Tse57d10_glc, mRNA sequence.

BX561724 Gl:33371526
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0
                                                                                                            BF582680 45 bp mRNA linear EST 12-DEC-2000 602094085F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4208373 5',
                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria, Rodentia, Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 45)
NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans and expression analysis of putative immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

Tissue Procurement: Jeffrey E. Green, M.D.

Tona Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

Plate: LiAM9712 row: j column: 22

High quality sequence stop: 45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        response genes
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Glossina morsitans morsitans
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Best Local Similarity 100.
Matches 33; Conservative
                                                                                                                                                                         mRNA sequence.
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DEFINITION

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RESULT 14 BX561724

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ORIGIN

ORGANISM

REFERENCE AUTHORS

TITLE

VERSION KEYWORDS SOURCE ACCESSION

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0;

/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN

Query Match 1.6%; Score 33; DB 14; Length 46; Best Local Similarity 100.0%; Pred. No. 0; Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps

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> Search completed: July 2, 2004, 07:35:58 Job time : 5412 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Description	11411	AX287571 Se	AX287575 8	AX287578 8	AAZB	AX287583	E62856 Se	BD01186	I29931 Se	AXI	E2O.		AX2	AX2	E50:	136	AR4232	AX2613	BD1186	BD118771 EST and	BD1704	AK3096	AX4430	AX4596	AR0388	AR4291	339 AX838339 Sequence	AX8408	BD0184	A43784		A62995 Sequence	70 AR1/9066	E04638 Synthesi		2 AX104902 Sequen	03 AX104903 Sequenc	73 AX474673	74 AX4/46/4 Sequenc	1	ALIGNMENTS			ďα	77390.					crimation utilizing primer extension
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Gaps

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Indels

PAT 21-NOV-2001

linear

DNA

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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Pl primer for use in allele discrimination"
                                                                                                                                                                                                                                                                            abarz A,P.
Process for allele discrimation utilizing primer extension
Parents for 1077390-A 25 18-OCT-2001;
Molecular Staging, Inc. (US)
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Local Similarity 100.0%; Pred. No. 9e-07;
es 34; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 9e-07;
tive 0; Mismatches 0;
                                           AX287582 46 bp
Sequence 25 from Patent WO0177390.
AX287582
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:33630"
/noTe="PI primer for use in allele discrimination"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        abarz A,P.
Process for allele discrimation utilizing primer extension
Patent: WO 0177390-A 21 18-OCT-2001;
Molecular Staging, Inc. (US)
Location/Qualifiers

    .45
    Organism="synthetic construct"
    /mol type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Pl primer for use in allele discrimination"

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1.6%; Score 34; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 9e-07;
Matches 34; Conservative 0; Mismatches 0;
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Sequence 18 from Patent WO0177390.
AX287575
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Sequence 21 from Patent WO0177390.
AX287578
AX287578.1 GI:17049344
            Location/Qualifiers
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AX287578/c
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AX287575/c
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/organism="synthetic construct"
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/db_tref="taxon:32630"
/noTe="PI primer for use in allele discrimination"
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Patent: WO 0177390-A 22 18-OCT-2001;
Molecular Staging, Inc. (US)
Location/Qualifiers
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      linear
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         DNA
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46 bp
Sequence 22 from Patent WO0177390.
AX287579
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PAT 02-AUG-2002

AX287583/c

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

FEATURES

Matches

ORIGIN

ACCESSION VERSION KEYWORDS

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SATO, SEITA SATO
OS Artificial Sequence
PN WO 00792820-A/13
PD 28-DEC-2000-A000 SEPP 22-JUN-2000 WO 20003PD04095
PF 22-JUN-1999 JP 99P 175928
PI ARADA, TOSHINORI SATO,
PI SEIYA SATO
PC GOIN33/569, C12N15/40
CC
FH Key Location/Qualifiers.
                                                                                                                                                                                                                          Detection kit for SRSV
Patent: WO 0079280-A 13 28-DEC-2000;
JAPAN AS REPRESENTED BY DIRECTOR GE YOSHIHIKO HIROSE, MITSUAKI MORIGUCHI, KIMIYASU ISOBE DISEASES, DENKA SEIKEN CO LTD, NAOKAZU TAKEDA, KATSURO NATORI, TATSUO MIYAMURA, KUNIO KAMATA, TOSHINORI
                                                                                                                                                                             1 (bases 1 to 33)
Takeda,N., Natori,K., Miyamura,T., Kunio, Kamata, Sato,T. and
                                                  linear
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100.0%; Pred. No. 1.1e-05;
tive 0; Mismatches 0; Indels
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Pickup,D.J., Patel,D. and Antczak,J.B. Site-specific RNA cleavage
Patent: US 5578468-A 44 26-NOV-1996;
Location/Qualifiers
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tive 0; Mismatches
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Sequence 44 from patent US 5578468.
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                                              33 bp
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/organism="unknown"
                                                                                           BD011883.1 GI:22092072
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18-APR-1996 US 08/634325
KENNETH JACOBS, JOHN M MCCOY, LISA A RACIE, EDWARD R LAVALLIE, PI
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Jacobs,K., Mccoy,J.M., Racie,L.A., Lavallie,E.R., Merberg,D. and
Spaulding,V.
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/mol_type="unassigned DNA"
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/note="Pl primer for use in allele discrimination"
                                                                                                                                                                   Process for allele discrimation utilizing primer extension Patent: WO 0177390-A 26 18-OCT-2001; Molecular Staging, Inc. (US) Location/Qualifiers
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Patent: JP 2001509004-A 14 10-JUL-2001;
GENETICS INSTITUTE INC
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   46 bp
Sequence 26 from Patent W00177390.
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C12N15/12, C07K14/47, A61K38/17
Strandedness: Double,
Topology: Linear; Location/Quali
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Petrik, J., Allain, J. and Pearson, G.J.
OLIGOMUCLEOTIDES AND THEIR USE
PATENT: WO 9603528-A 6 08-FEB-1996;
LYNXVALE LTD (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.5%; Score 32; DB Best Local Similarity 100.0%; Pred. No. 1.1 Matches 32; Conservative 0; Mismatches
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Patent: US 6457426-A 7 01-OCT-2002;
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Location/Qualifiers
0; Mismatches

    .40
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/mol_type="unassigned DNA"
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Sequence 7 from patent US 6457426.
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Sequence 7 from Patent WO0161033.
AX225198
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Sequence 6 from Patent WO9603528.
A48799
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E 1 (bases 1 to 38)
Obara,M., Obara,K., Tabira,K., Matsuzaki,J. and Om,H.
Vector expressing full-length gene of RNA virus and utilization
Vector expressing full-length gene of RNA virus and utilization
Datent: JP 2001152793-A 19 06-JUN-2000;
TOKYO METROPOLITAN ORGANIZATION FOR MEDICAL RESEARCH, CHUGAI
PHARMACEUT CO LTD
OS Artificial sequence
PN JP 2000152793-A/19
PD 06-JUN-2000
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                                                                                                                                                                                                                                  Blanco, D.L., bernad Miana, A., dominguez Lopez, O. and garcia Diaz, M. Dna polymerase lambda and uses thereof Patent: WO 0125442A 25 12-APR-2001; CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS (ES) Location/Qualifiers
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CIZN15/09,A01K67/027,C12N5/10,C12Q1/70,C12N15/00,C12N5/00 CC
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                                                                                        AX106972 37 bp 37 bb 25 from Patent W00125442. AX106972.1 GI:13922521
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1. .43
/organism="synthetic construct"
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                                                                                        Schouten, J.P.
Multiplex ligatable probe amplification
Patent: Wo 0161033-A 7 23-Aug-2001;
Schouten, Johannes Petrus (NL)
Location/Qualifiers
 AX225198.1 GI:15555219
                              synthetic construct
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PAT 30-AUG-2001 linear 2067 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098 DNA 43 AAAAAAAAAAAAAAAAAAAAAAAAAA 12 AX206861 44 bp Sequence 7 from Patent WO0155391. AX206861 Ωp

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Jakobovits, A., Afar, D.E., Challita-Eid, P.M., Levin, E.,
Mitchell, S.C. and Hubert, R.S.
84029: a prostate and testis specific protein highly expressed in
prostate cancer.
Patent: WO 0155391-A 7 02-AUG-2001;
Urogenesys, Inc. (US) AUTHORS TITLE

JOURNAL FEATURES

1. .44
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/noTe="Primer" source

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1.5%; Score 32; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
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US-09-445-223-2 Perfect score: Sequence:

OLIGO_NUC Gapop_60.0 , Gapext 60.0 Scoring table:

3373863 seqs, 2124099041 residues Searched:

0 Word size

3185356 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

geneseqn2001as:*
geneseqn2001bs:*
geneseqn2002s:*
geneseqn2003as:* N_Geneseq_29Jan04:* geneseqn1980s:*
geneseqn1990s:*
geneseqn2000s:* geneseqn2003bs:* geneseqn2003cs:* geneseqn2004s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Abz04660 Himan	Allela	Allele		Allele			ı v	7 RNA	25 RNA	ם [[ע כ	פופווע א	.	1		ט ט	ט י	י ר	·	4 nepati	٠,	2000	ı m
	ID	ABZ04660	AAS95728	AAS95724	AAS95735	AAS95731	ABK99273	ABK99272	AAD27116	AAD27117	AAD27125	AAS95732	AAS95736	AAV02146	AATBRORD	AAN70278	AAN92244	ADC33445	AAF29153	AAZ57404	AAL07487	AA025031	AAZ98722	AAA39649
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AAD17216	AAV09273	AAS11665	ADD33791	AAF26960	AAL07489	AAT04081	ABK30210	ADD31868	AAQ66922	AAV37933	AAF60897	AAS58336	ABK30194	ABN89414	ABQ77278	ADA18497	ADC56860	ADC56857	ADC56856	AAD27124	AAV03013
4	~	2	6	4	4	~	9	σı	7	7	4	4	9	9	7	7	σ	σ	σ	9	7
43	44	44	44	45	47	48	48	48	20	20	20	20	20	20	20	20	20	20	20	37	41
1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5
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ALIGNMENTS

RESULT 1

17; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe; Human leukocyte gene expression profiling probe SEQ ID NO 4651. ABZ04660 standard; DNA; 50 BP. (first entry) 09-JAN-2003 ABZ04660; ABZ04660

Homo sapiens.

WO200257414-A2.

25-JUL-2002.

22-OCT-2001; 2001WO-US047856.

20-OCT-2000; 2000US-0241994P. 08-JUN-2001; 2001US-0296764P.

(BIOC-) BIOCARDIA INC.

Phillips J; Prentice J, Altman P, P, nuth J, Fry K, Matcuk G, A Woodward R, Quertermous T, Wohlgemuth J,

WPI; 2002-636525/68.

New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.

Claim 1; Page 476; Opp; English.

The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient,

disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes, obesity, cancers of the head, neck, skin, brain, oesophagus, stomach, lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma and melanoma. Sequences AAS95711-AAS95745 represent primers, targets and

fluorescence decorators used in the detection of RCA products

888888

Sequence 45 BP; 2 A; 5 C; 0 G; 38 T; 0 U; 0 Other;

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.; 0

Length 45;

1.6%; Score 34; DB 6; I

Best Local Similarity

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Query Match

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predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, liver allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosur rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
                                                                                                                                                                                                                                                                                                                                                                                Rolling circle amplification; single nucleotide polymorphism; anaemia; exonuclease deficient DNA polymerase; amplification target circle; RCA; Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss; Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis; diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach; lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma; melanoma; PCR primer; sequencing primer; probe.
                                                                                                                                            Gaps
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                                                                                                                                                                                                 1 TGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGATCACCATCT
                                                                                                                 2.4%; Score 50; DB 6; Length 50; 100.0%; Pred. No. 3.2e-09; tive 0; Mismatches 0; Indels
                                                                                     Sequence 50 BP; 10 A; 13 C; 10 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                        1803 IGGGICTICAGCCTTACCCGGAAATACTTGTGGT
                                                                                                                                                                                                                                                                                                                                                          Allele discrimination P1 primer #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLE-) MOLECULAR STAGING INC
                                                                                                                                                                                                                                                                         AAS95728 standard; DNA; 45 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-APR-2000; 2000US-0194843P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-2001; 2001WO-US011151.
                                                                                                                                                                                                                                                                                                                                 14-FEB-2002 (first entry)
                                                                                                               Query Match
Best Local Similarity 100.
Matches 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                            AAS95728/c
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The invention relates to detecting single nucleotide polymorphisms by contacting an allele-specific oligonuclectide primer (P1) with a target contacting an allele-specific oligonuclectide primer (P1) with a target complementary to P1 at one end but the terminal nuclectide and the complementary to P1 at one end but the terminal nuclectide and the chiral nuclectide from the terminal at the other end of P1 may not be complementary. The complex is then contacted with an exonuclease complementary as the remmandary conditions that promote extension of P1 with the target DNA as the template, thereby forming an extended segment of P1. Oligonucleotide probes hybridising to one or more target CC segment of P1. Oligonucleotide probes hybridising to one or more target concluded mismatch. Primer sequences complementary to a sequence on an nucleotide mismatch. Primer sequences complementary to a sequence on an multication target circle can be used in rolling circle amplification (CRA). The method is useful for diagnosing a disease caused by, induced to by or related to a mutation in at least one gene, such as Parkinson's disease, polycystic kidney disease, Tay-Sachs disease, Huntington
                                                                                                                                                                                                                                                                                                                                                                                         Rolling circle amplification; single nucleotide polymorphism; anaemia; exonuclease deficient DNA polymerase; amplification target circle; RCA; Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; BS; Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis; diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach; lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma; melanoma; PCR primer; sequencing primer; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting single nucleotide polymorphism involves amplifying target sequences using small primer probe that matches or mismatches to target sequence and extending primer probe which is then detected.
                        Gaps
                           0; Indels
                                                                     2065 Т<u>СВАВАВАВАВАВАВАВАВАВАВАВАВАВ</u> 2098
                                                                                                          37 TGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4
100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                                           Allele discrimination P1 primer #8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR STAGING INC.
                                                                                                                                                                                                                               AAS95724 standard; DNA; 45 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-2000; 2000US-0194843P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-APR-2001; 2001WO-US011151
                                                                                                                                                                                                                                                                                                                (first entry)
                               34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200177390-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Abarzua P;
                                                                                                                                                                                                                                                                          AAS95724;
                                                                                                                                                                                                           AAS95724/c
                                    Matches
                                                                                                                                                                                      RESULT 3
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The invention relates to detecting single nucleotide polymorphisms by contacting an allele-specific oligonucleotide primer (P1) with a target contacting an allele-specific oligonucleotide primer (P1) with a target contacting an allele-specific oligonucleotide primer (P1) with a target sequence to somplementary to P1 at one end but the terminal nucleotide and the third nucleotide from the terminal at the other end of P1 may not be complementary. The complex is then contacted with an exonuclease of efficient DNA polymerase enzyme under conditions that promote extension of P1 with the target DNA as the template, thereby forming an extended segment of P1. Oligonucleotide probes hybridising to one or more target the absence of sequence amplification indicates the presence of a single uncleotide mismatch. Primer sequences complementary to a sequence on an uncleotide mismatch. Primer sequences complementary to a sequence on an amplification target circle can be used in rolling circle amplification (RCA). The method is useful for diagnosing a disease caused by, induced by or related to a mutation in at least one gene, such as Parkinson's disease, polycystic kidney disease, Tay-Sachs disease, Huntington

Detecting single nucleotide polymorphism involves amplifying target sequences using small primer probe that matches or mismatches to target sequence and extending primer probe which is then detected.

WPI; 2002-049157/06.

Abarzua P;

Claim 15; Page 41; 67pp; English.

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disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes, obesity, cancers of the head, neck, skin, brain, oesophagus, stomach, lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma a melanoma. Sequences AAS95711-AAS95745 represent primers, targets and
                                                                                                     fluorescence decorators used in the detection of RCA products
555555×8
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and

Sequence 45 BP; 1 A; 6 C; 0 G; 38 T; 0 U; 0 Other;

Gaps . 1.6%; Score 34; DB 6; Length 45; 0; Indels Pred. No. 0.0044; 100.0%; Preq. w. 34; Conservative Query Match Best Local Similarity Matches

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2065 TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098

AAS95735/c RESULT

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AAS95735 standard; DNA; 46 BP AAS95735; Allele discrimination Pl primer #19.

(first entry)

14-FEB-2002

Rolling circle amplification; single nucleotide polymorphism; anaemia; exonuclease deficient DNA polymerase; amplification target circle; RCA; parkinson; a disease; polycystic kidney disease; Tay-Sachs disease; ss; Huntington disease; sickle cell anaemia; haemophilia; yystic fibrosis; diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach, lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma; melanoma; PCR primer; sequencing primer; probe.

Homo sapiens.

WO200177390-A2

18-OCT-2001.

05-APR-2001; 2001WO-US011151

05-APR-2000; 2000US-0194843P.

(MOLE-) MOLECULAR STAGING INC.

Abarzua P;

WPI; 2002-049157/06.

Detecting single nucleotide polymorphism involves amplifying target sequences using small primer probe that matches or mismatches to target sequence and extending primer probe which is then detected.

Claim 15; Page 42; 67pp; English.

The invention relates to detecting single nucleotide polymorphisms by contacting an allele-specific oligonucleotide primer (PI) with a target contacting an allele-specific oligonucleotide primer (PI) with a target polymucleotide to form a hybridisation complex, where the target sequence is complementary to plat one end but the terminal nucleotide and the the complementary. The complex is then contacted with an exonuclease complementary. The complex is then contacted with an exonuclease of PI with the target DNA as the template, thereby forming an extended of PI with the target DNA as the template, thereby forming an extended complex is the complex in the proper of a single complex in the proper of sequence amplification indicates the presence of a single contacted mismatch. Primer sequences complementary to a sequence on an uncleotide mismatch. Primer sequences complementary to a sequence on an expalification target circle can be used in rolling circle amplification (RCA). The method is useful for diagnosing a disease caused by, induced by or related to a mutation in at least one gene, such as Parkinson's disease, polycystic kidney disease, Tay-Sachs disease, Huntington

disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes, obesity, cancers of the head, neck, skin, brain, oesophagus, stomach, lung, breast, colon, ovary, testis or prostate, levksemia, lymphoma a melanoma. Sequences AAS9711-AAS95745 represent primers, targets and fluorescence decorators used in the detection of RCA products 8888888

Sequence 46 BP; 2 A; 4 C; 0 G; 40 T; 0 U; 0 Other;

Length 46; 0; Indels Score 34; DB 6; 1 Pred. No. 0.0043; 1.6%; Score 34; DB 100.0%; Pred. No. 0.0 ative 0; Mismatches Query Match
Best Local Similarity 100..
Best Local 34; Conservative

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Gaps

. 0

2065 TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098 34 TGAAAAAAAAAAAAAAAAAAAAAAAAAA 1 Š g

AAS95731/c RESULT 5

AAS95731 standard; DNA; 46

AAS95731;

14-FEB-2002 (first entry)

Allele discrimination P1 primer #15.

Rolling circle amplification; single nucleotide polymorphism; anaemia; exonuclease deficient DNA polymerase; amplification target circle; RCA; Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss; Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis; diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach; nung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma; melanoma; PCR primer; sequencing primer; probe.

Homo sapiens.

WO200177390-A2.

18-OCT-2001

05-APR-2001; 2001WO-US011151.

05-APR-2000; 2000US-0194843P.

MOLE-) MOLECULAR STAGING INC

Abarzua P;

WPI; 2002-049157/06.

Detecting single nucleotide polymorphism involves amplifying target sequences using small primer probe that matches or mismatches to target sequence and extending primer probe which is then detected.

Claim 15; Page 42; 67pp; English.

The invention relates to detecting single nucleotide polymorphisms by contacting an allele-specific oligonucleotide primer (PI) with a target contacting an allele-specific oligonucleotide primer (PI) with a target contacting an allele-specific oligonucleotide primer (PI) with a target sequence is complementary to PI at one end but the terminal nucleotide and the confirmation of PI may not be complementary. The complex is then contacted with an exonuclease complementary. The complex is then conditions that promote extension of PI with the target DNA as the termplate, thereby forming an extended of PI with the target DNA as the termplate, thereby forming an extended contact of PI oligonucleotide probes hybridising to one or more target polymucleotides distinguish between matched and mismatched 3 and single conclude mismatch. Primer sequences complementary to a sequence on an uncleotide mismatch. Primer sequences complementary to a sequence on an emplification target circle can be used in rolling circle amplification (RCA). The method is useful for diagnosing a disease caused by, induced the presence of a mutation in at least one gene, such as Parkinson's disease, polycystic kidney disease, Tay-Sachs disease, Huntington

templates

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ö
       obesity, cancers of the head, neck, skin, brain, oesophagus, stomach, lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma and melanoma. Sequences AAS95711-AAS95745 represent primers, targets and fluorescence decorators used in the detection of RCA products
sickle cell anaemia, haemophilia, cystic fibrosis, diabetes,
                                                                                    Gaps
                                                                                    ..
                                                                   Length 46;
                                                                                   Indels
                                                  Sequence 46 BP; 3 A; 4 C; 0 G; 39 T; 0 U; 0 Other;
                                                                  Query Match 1.6%; Score 34; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 34; Conservative 0; Mismatches 0;
                                                                                                     2065 ТСАРАРАРАРАРАРАРАРАРАРАРАРАРАРАРА
                                                                                                                     34 TGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
                                                                                                                                                                ABK99273 standard; RNA; 36 BP
                                                                                                                                                                                                   21-OCT-2002 (first entry)
                                                                                                                                                                                  ABK99273;
                                                                                                                                                  RESULT 6
                                                                                                                                                           ABK99273
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   8X333333
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Novel replicase complex comprising hepatitis C virus NSSB replicase, a 3 nucleotide-long template to which a 2 nucleotide-long primer is annealed, and template and primer which do not form a stable duplex in the absence 07-APR-2000; 2000US-0195852P. Ferrari E; 06-APR-2001; 2001US-00828034 PI; 2002-582330/62. HONG Z. FERRARI E. Zhong W, Hong Z, ZHON/) ZHONG W. 30-MAY-2002. FERR/) HONG/)

of HCV NS5B

The invention relates to a replicase complex comprising a hepatitis C virus (HCV) NS5B replicase protein, a linear nucleic acid template and a complementary nucleic acid primer which is annealed to the 3' terminus of complementary nucleic acid primer which is annealed to the 3' terminus of complementary nucleic acid primer as the template and primer do not primer is two or three nucleotides, and the template and primer do not primer is useful for detecting HCV replicase activity and permits catablishment of sensitive RNA-dependent RNA polymerase assays to screen and evaluate antiviral inhibitors and to improve the specificity and a reliable system for determining kinetic and thermodynamic constants of a reliable system for determining kinetic and thermodynamic constants of HCV NS5B-catalysed nucleotide incorporation and investigation of Specifically, the short RNA template and primer pairs are useful in sorreming assays which are used for determining kinetic, thermodynamic and mechanistic properties of NS5B replication and ultimately in the development of inhibitors of NS5B replication and ultimately in the development of inhibitors of NS5B replication and ultimately in the specifically may be used for developing anti-HCV pharmaccuticals. Sequences ABK99271-ABK99296 represent HCV NS5B replicase RNA synthesis Example; Page 6; 17pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                        Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3 nucleotide-long template to which a 2 nucleotide-long primer is annealed, and template and primer which do not form a stable duplex in the absence
                                                    Gaps
                                                                                                                                                                                                    Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #2.
                                                    ô
                                                                                                                                                                                                                        Hepatitis C virus; HCV; NS5B replicase; 88; RNA polymerase.
                                Query Match 1.6%; Score 33; DB 6; Length 36; Best Local Similarity 100.0%; Pred. No. 0.011; Matches 33; Conservative 0; Mismatches 0; Indels
             Sequence 36 BP; 33 A; 0 C; 2 G; 0 T; 1 U; 0 Other;
                                                                        2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
                                                                                        2 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Page 6; 17pp; English.
                                                                                                                                            ABK99272 standard; RNA; 36 BP
                                                                                                                                                                                                                                                                                                                                                                                     Ξ
                                                                                                                                                                                                                                                                                                                           07-APR-2000; 2000US-0195852P.
                                                                                                                                                                                                                                                                                                       06-APR-2001; 2001US-00828034
                                                                                                                                                                                                                                                                                                                                                                                    Zhong W, Hong Z, Ferrari
                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-582330/62.
                                                                                                                                                                                                                                                                                                                                                         (HONG/) HONG Z.
(FERR/) FERRARI E.
                                                                                                                                                                                                                                                                                                                                               ZHON/) ZHONG W.
                                                                                                                                                                                                                                                                 US2002064771-A1.
                                                                                                                                                                                      21-OCT-2002
                                                                                                                                                                                                                                                                                     30-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          of HCV NS5B
                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                   ABK99272;
                                                                                                                            RESULT 7
                                                                                                                                     ABK99272
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Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #3.

Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase.

JS2002064771-A1

Synthetic.

The invention relates to a replicase complex comprising a hepatitis C virus (HCV) NSB replicase protein, a linear nucleic acid template and a complementary nucleic acid primer which is annealed to the 3' terminus of the template, where the template is at least three nucleotides and the primer is two or three nucleotides, and the template and primer do not primer is two or three nucleotides, and the template and primer do not form a stable duplex in solution in the absence of the HCV NSBB protein. The complex is useful for detecting HCV replicase activity and permits catablishment of sensitive RNA-dependent RNA polymerase assays to screen and evaluate antiviral inhibitors and to improve the specificity and complex is also useful in the development of a reliable system for determining kinetic and thermodynamic constants of HCV NSSB-catalysed nucleotide incorporation and investigation of screening assays which are used for determining kinetic, thermodynamic screening assays which are used for determining kinetic, thermodynamic conference and mechanistic properties of NSSB replication and ultimately in the capical component of inhibitors of NSSB replication and ultimately in the reminister of inhibitors of NSSB replication and ultimately in the reminister of and mechanistic MSSB. Newly identified inhibitors of replicase activity may be used for developing anti-HCV pharmaceuticals. emplates

Sequence 36 BP; 34 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

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Gaps
                                 ٥:
       Score 33; DB 6; Length 36;
Pred. No. 0.011;
0; Mismatches 0; Indels
1.6%; Scot.
100.0%; Pred. No. ...
0; Mismatches
                             33; Conservative
                  Similarity
       Query Match
                  Best Local
                            Matches
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2066 СААВАВАВАВАВАВАВАВАВАВАВАВАВАВАВА

·.

RESULT 8

AAD27116

AAD27116 standard; RNA; 36 BP

AAD27116;

(first entry) 09-APR-2002

RNA template, AA used to direct RNA synthesis by HCV RNA polymerase.

Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B; lead compound; RNA polymerase; ss.

Unidentified

US6322966-B1

27-NOV-2001.

99US-00309670. 11-MAY-1999;

99US-00309670. 11-MAY-1999;

(ZHON/) ZHONG W.

HONG Z. (HONG/)

(LAUJ/) LAU J Y N.

Lau JYN; Zhong W, Hong Z,

WPI; 2002-096587/13.

Assay system for hepatitis C virus replicase activity comprises RNA template with unstable, small stemloop capable of forming copy-back structure, viral non-structural protein 5B, nucleoside triphosphates,

Example 1; Fig 1A; 10pp; English.

The present invention relates to an assay system for hepatitis C virus (HCV) replicase activity. The assay system comprises an RNA template that has an unstable, small stemloop at the 3' end capable of forming a copyback structure, a HCV non-structural protein 5B (NSSB), ARP, GTP, CTP, radiolabelled and an assay buffer that supports replication activity of NSSB. The invention also relates to the identification of optimal properties of an RNA template for copy-back self-priming RNA synthesis of HCV. This activity can be used to screen for anti-HCV replicase compounds or characterise the biological relevance of lead compounds. The Optimal RNA templates can be used for developing a system to characterise the biological relevance of lead compounds. The Optimal RNA templates can be used for developing a system to characterise mechanistically and kinetically, and for developing a system to characterise HCV NSSB polymerase mechanistically and kinetically and for designing small RNA molecules to co-crystallise with HCV NSSB polymerase. The assay system of the invention is useful for detecting HCV replicase activity. The nucleic acid synthesised by NSSB is detected by evaluating an autoradiograph of reaction products separated by syllating an present sequence is RNA template, AA used to direct RNA synthesis by RNA polymerase proteins of HCV, BVDV and polivirus. This sequence is used in the exemplification of the invention

Sequence 36 BP; 34 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

Gaps .. 1.6%; Score 33; DB 6; Length 36; 100.0%; Pred. No. 0.011; tive 0; Mismatches 0; Indels Query Match 1.6 Best Local Similarity 100. Matches 33; Conservative

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2066 САВАВАВАВАВАВАВАВАВАВАВАВАВАВАВА 2098
                                    2 СААВАВАВАВАВАВАВАВАВАВАВАВАВАВА 34
                            qq
ò
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AAD27117 standard; RNA; 36

AAD27117;

09-APR-2002 (first entry)

RNA template, AU used to direct RNA synthesis by HCV RNA polymerase.

Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B; lead compound; RNA polymerase; ss.

Unidentified

US6322966-B1

27-NOV-2001.

11-MAY-1999;

99US-00309670.

99US-00309670

11-MAY-1999;

(ZHON/) ZHONG W.

HONG Z. (HONG/)

(LAUJ/) LAU JYN.

Zhong W, Hong Z, Lau JYN;

WPI; 2002-096587/13.

Assay system for hepatitis C virus replicase activity comprises RNA template with unstable, small stemloop capable of forming copy-back structure, viral non-structural protein 5B, nucleoside triphosphates, buffer.

Example 1; Fig 1A; 10pp; English.

The present invention relates to an assay system for hepatitis C virus (HCV) replicase activity. The assay system comprises an RNA template that has an unstable, small stemloop at the 3' end capable of forming a copyback structure, a HCV non-structural protein SB (NSSB). AIP, GTP, CTP, and UTP nucleoside triphosphates (MTPS), where one of the NTP is cridiolabelled and an assay buffer that supports replication activity of NSSB. The invention also relates to the identification of optimal corporations also relates to the identification of optimal corporations of an RNA template for copy-back self-priming RNA synthesis of HCV. This activity can be used to soreen for anti-HCV replicase compounds or to characterise the biological relevance of lead compounds. The COPTIMENT RNA templates can be used for developing a system to characterise CC optimal RNA templates can be used for developing a system to characterise CC will RNA molecules to co-crystallise with HCV NSSB polymerase. The assay system of the invention is useful for detecting HCV replicase activity. The nucleic acid synthesised by NSSB is detected by evaluating an autoradiograph of reaction products separated by evaluating an corporating and products separated by evaluating an products separated by evaluating an the averantificant of HCV, RNASH cuplates, AU used to direct RNA synthesis by RNA the averantificant of the invention of HCV, RNASH polymerase proteins of HCV, RNASH and polivirus. This sequence is used in polymerase proteins of HCV, BVDV and the exemplification of the invention

Sequence 36 BP; 33 A; 0 C; 2 G; 0 T; 1 U; 0 Other;

1.6%; Score 33; DB 6; Length 36; 100.0%; Pred. No. 0.011; live 0; Mismatches 0; Indels Query Match Best Local Similarity 100. Matches 33; Conservative

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Gaps

. 0

2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098 **САААААААААААААААААААААААААААА**

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Rolling circle amplification; single nucleotide polymorphism; anaemia; exonuclease deficient DNA polymerase; amplification target circle; RCA; Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss; Huntington disease; sickle cell anaemia, haemophilia; cystic fibrosis; diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach; lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma; melanoma; PCR primer; sequencing primer; probe.

Allele discrimination P1 primer #16.

(first entry)

14-FEB-2002

AAS95732;

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RNA template, (AU)2 used to direct RNA synthesis by HCV RNA polymerase.
                                                                                                                                                                                                                                                                                            Assay system for hepatitis C virus replicase activity comprises RNA template with unstable, small stemloop capable of forming copy-back structure, viral non-structural protein 5B, nucleoside triphosphates,
                                                                                           Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 37 BP; 33 A; 0 C; 2 G; 0 T; 2 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in the exemplification of the invention
                                                                                                      lead compound; RNA polymerase; ss
                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 2A; 10pp; English.
                 AAD27125 standard; RNA; 37 BP.
                                                                                                                                                                                99US-00309670.
                                                                                                                                                                                                  99US-00309670.
                                                                                                                                                                                                                                                           Lau JYN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA polymerase proteins of
                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                             WPI; 2002-096587/13
                                                                                                                                                                                                                               (HONG/) HONG Z. (LAUJ/) LAU J Y N.
                                                                                                                                                                                                                                                          Zhong W, Hong Z,
                                                                                                                                                                                                                     ZHON/) ZHONG W.
                                                                                                                                                                                                 11-MAY-1999;
                                                                                                                                            US6322966-B1
                                                                                                                                                                                11-MAY-1999;
                                                        09-APR-2002
                                                                                                                                                              27-NOV-2001.
                                     AAD27125;
RESULT 10
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Detecting single nucleotide polymorphism involves amplifying target sequences using small primer probe that matches or mismatches to target sequence and extending primer probe which is then detected.

(MOLE-) MOLECULAR STAGING INC.

WPI; 2002-049157/06.

Abarzua P;

05-APR-2001; 2001WO-US011151. 05-APR-2000; 2000US-0194843P.

WO200177390-A2 Homo sapiens.

18-OCT-2001

```
The present invention relates to an assay system for hepatitis C virus

(HCV) replicase activity. The assay system comprises an RNA template that

has an unstable, small stemloop at the 3' end capable of forming a copy-
back structure, a HCV non-structural protein 58 (NSSB), ATP, GTP, GTP,

c and UTP nucleoside triphosphates (NTPB), where one of the NTP is

radiolabelled and an assay buffer that supports replication activity of

NSSB. The invention also relates to the identification of optimal

properties of an RNA template for copy-back self-priming RNA synthesis of

HCV. This activity can be used to screen for anti-HCV replicase compounds

or to characterise the biological relevance of lead compounds. The

optimal RNA templates can be used for developing a system to characterise

CHCV NSSB polymerase mechanistically and kinetically and for designing

small RNA molecules to co-crystallise with HCV NSSB polymerase. The assay

CC system of the invention is useful for detecting HCV replicase activity.

The nucleic acid synthesised by NSSB is detected by evaluating an

constant sequence is RNA template, (AU) sused to direct RNA synthesis by

present sequence is RNA template, (AU) sused to direct RNA synthesis by

Dans an experience is RNA template, (AU) such invite manner of a used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HCV, BVDV and polivirus. This sequence is used
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                               Gaps
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      Score 33; DB 6; Length 37;
Pred. No. 0.011;
0; Mismatches 0; Indels
                                                        2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
                                                                               сававававававававававававававава 34
1.6%; Scor.
100.0%; Pred. No. v.
                                 33; Conservative
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Matches

5732/c AAS95732 standard; DNA; 46 BP.

RESULT 11

AAS95732

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The invention relates to detecting single nucleotide polymorphisms by contacting an allele-specific oligonucleotide primer (P1) with a target contacting an allele-specific oligonucleotide primer (P1) with a target polynucleotide to form a hybridisation complex, where the target sequence is complementary to plat one end but the terminal nucleotide and the third nucleotide from the terminal at the other end of P1 may not be complementary. The complex is then contacted with an exonuclease complementary as the template, thereby forming an extended of P1 with the target DNA as the template, thereby forming an extended segment of P1. Oligonucleotide probes hybridising to one or more target polynucleotides distinguish between matched and mismatched 3' ends, hence the absence of sequence amplification indicates the presence of a single uncleotide mismatch. Primer sequences complementary to a sequence on an explication target circle can be used in rolling circle amplification amplification in at least one gene, such as Parkinson's disease, polycystic kidney disease, Tay-Sachs disease, Huntington disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes, cobesity, cancers of the head, neck, skin, brain, osesophagus, stomach, and promers and primers, targets and melanoma. Sequences AMSSTV11. Expresent primers, targets and
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 33; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 46 BP; 2 A; 3 C; 0 G; 41 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2066 GAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; Page 42; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS95736 standard; DNA; 46 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS95736/c
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Allele discrimination P1 primer #20.
   (first entry)
   14-FEB-2002
 AAS95736;
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Rolling circle amplification; single nucleotide polymorphism; anaemia; exonuclease deficient DNA polymerase; amplification target circle; RCA; Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss; Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis; diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach; lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma; melanoma; PCR primer; sequencing primer; probe.

Homo sapiens.

WO200177390-A2.

18-OCT-2001

05-APR-2001; 2001WO-US011151.

05-APR-2000; 2000US-0194843P.

(MOLE-) MOLECULAR STAGING INC

Abarzua P;

WPI; 2002-049157/06.

Detecting single nucleotide polymorphism involves amplifying target sequences using small primer probe that matches or mismatches to target sequence and extending primer probe which is then detected.

Claim 15; Page 43; 67pp; English.

The invention relates to detecting single nucleotide polymorphisms by contacting an allele-specific oligonucleotide primer (Pl) with a target contacting an allele-specific oligonucleotide primer (Pl) with a target control control edited to form a hybridisation complex, where the target sequence is complementary to Pl at one end but the terminal nucleotide and the complementary. The complex is then contacted with an exonuclease complementary. The complex is then contacted with an exonuclease of Pl with the target DNA as the template, thereby forming an extended segment of Pl with the target DNA as the template, thereby forming an extended segment of Pl oligonucleotide probes hybridising to one or more target the absence of sequence amplification indicates the presence of a single concleotide mismatch. Primer sequences complementary to a sequence on an uncleotide mismatch. Primer sequences complementary to a sequence on an explication in at least one gene, such as Parkinson's disease, polyoystic kidney disease, Tay Sachs disease, Huntington concleoses, polyoystic kidney disease, Tay Sachs disease, Huntington consent, cancers of the head, neck, skin, brain, osesophagus, stomach, concludy breast, colon, ovary, testis or prostate, leukaemia, lymphoma and flux anoma sequences AAS95711-AAS95745 represent primers, targets and flux and an anoma sequences are prepresent primers, targets and flux and an anoma sequences and the head. quences AAS95711-AAS95745 represent primers, targe decorators used in the detection of RCA products

Sequence 46 BP; 1 A; 3 C; 0 G; 42 T; 0 U; 0 Other;

DB 6; Length 46; Indels 0 0.01; 1.6%; Scor. 100.0%; Pred. No. v. 0; Mismatches Conservative Similarity 33; Query Match Local Matches

2066 GАААААААААААААААААААААААААААААА **СААРАРАРАРАРАРАРАРАРАРАРАРАРАРАРАРА** 38

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RESULT 13
AAV02146
ID AAV02

AAV02146 standard; cDNA; 49 BP

(first entry) 12-MAY-1998 AAV02146

Human secreted protein AK533 3' portion including the polyA tail.

Human; secreted protein; ATCC 98026; cytokine; immunomodulation; cell proliferation; differentiation; regulation; ds.

Homo sapiens

WO9739123-A2

23-OCT-1997.

97WO-US006139. 14-APR-1997;

96US-00634325 18-APR-1996;

(GEMY) GENETICS INST INC

Merberg D; Lavallie ER, Racie LA, Mccoy JM, Spaulding V; Jacobs K,

WPI; 1997-526460/48.

possibly secreted proteins encoded clones present in ATCC 98026 - poing cytokine, cell proliferation/differentiation regulating having cytokine, cell proliferation/differen immunomodulating and many other activities.

Disclosure; Page 86; 139pp; English.

The present sequence encodes a portion of a novel human secreted protein deposited under accession number ATCC 98026. The secreted protein can be used to determine biological activity, to raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that have a very wide range of biological activities although no evidence for any is provided in the specification. Typical of these are cytokine, cell cytokines; immunostimulating/immunosuppressant activities (e.g. for treating human immunodial dimmonsuppressant activities (e.g. for treating an allergy); regulation of haematopoiesis (e.g. for treating anamia or as adjunct to chemotherapy); stimulation of growth of bone, carcilage, tendons, ligaments and/or nerves (e.g. for treating wounds, cartilage, tendons, ligaments and/or nerves (e.g. for treating wounds, crimilation of follicle stimulating hormone (for control of fertility) tumours); haemostatic or thrombolytic activity (e.g. for treating corrections, chaemotatic and chemokinetic activity (e.g. for treating septic shock, Chun's disease; for treating infections, chaemotating septic shock, Chun's disease; for treating corresponding nucleic activity disease; for requilation of treating psoriasis or other hyperproliferative disease; for requilation of many others. Also contemplated is the use of the corresponding nucleic acid in gene therapy procedures

Sequence 49 BP; 40 A; 2 C; 6 G; 1 T; 0 U; 0 Other;

. 0 1.6%; Score 33; DB 2; Length 49; 100.0%; Pred. No. 0.01; 0; Indels 100.0%; Prec. ... 33; Conservative Similarity Query Match Best Local 9 Matches

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Gaps

2066 САВАВАВАВАВАВАВАВАВАВАВАВАВАВАВАВ 2098

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Gaps

.; 0

AAT88080 standard; cDNA; 49 BP. RESULT 14 AAT88080 SAXA

AAT88080,

86EP-00116906

04-DEC-1986;

08-JUL-1987 EP227976-A.

(first entry)

14-MAY-1998

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The present sequence is the 3' portion of a cDNA clone encoding a human secreted protein, which may have nutritional uses, or cytokine and cell coliferation/differentiation, immune stimulating or suppressing, proliferation/differentiation, immune stimulating or suppressing, haematopoiesis regulating, tissue growth, activin/inhibin, cenemicatic/chemokinetic, haemostatic and thrombolytic, receptor/ligand, chemoteric/chemokinetic, haemostatic and thrombolytic, receptor/ligand, anti-inflammatory or tumour inhibition activities. It can also be used to compare the cone Apilo was let isolated from a human adult placenta cDNA clone Apilo.

Con Anti-inflammatory or treat diseases/disorders related to its function. The partial cDNA clones Am331, AM610, AM340, AM282, AK647, Clibrary. The partial cDNA clones H617 and BB9 were lst isolated from a human foetal kidney cDNA human peripheral blood monocyte cell (Thi or Th2) cDNA library. The partial cDNA clones H617 and BB9 were lst isolated from a human ovary (BA-1) cDNA library. The partial cDNA clones AS34 and AS32 were lst isolated from a human flowed brain cDNA clones AS34 and AS32 were lst isolated from a human adult retina cDNA library. The partial cDNA clones AS34 and AS32 were lst isolated from a human adult retina cDNA library. The partial cDNA clones AS34 and AS32 were lst isolated from a human adult retina cDNA library. The partial cDNA clones AS34 and AS32 were lst isolated from a human adult retina cDNA library. The partial cDNA clones AS34 and AS32 were lst isolated from a murine bone marrow (stromal cell cline FCM-4) cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human and murine secreted proteins - useful in research or treatment of diseases or disorders related to their function.
                                                                            Human; secreted protein; research; treatment; AM533; 3' portion; ds.
                                  3' portion of cDNA clone encoding secreted protein AK533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 86; 140pp; English
                                                                                                                                                                                                                                                                                                                          96US-00631184.
                                                                                                                                                                                                                                                                           97WO-US006042
                                                                                                                                                                                                                                                                                                                                                                           (MURO-) MURO PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-526459/48.
                                                                                                                                                                                                                                                                                                                                                                                                                            Theoharides TC;
                                                                                                                                                                                                                                                                                11-APR-1997;
                                                                                                                                                                                                                                                                                                                               12-APR-1996;
                                                                                                                                         Homo sapiens
                                                                                                                                                                                        WO9739122-A2
                                                                                                                                                                                                                                    23-0CT-1997.
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#X#X#X8X#X#X#X#X#X#X#X##X##X
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                                                                     Gaps
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                                 ch 1.6%; Score 33; DB 2; Length 49; l Similarity 100.0%; Pred. No. 0.01; 33; Conservative 0; Mismatches 0; Indels
Sequence 49 BP; 40 A; 2 C; 6 G; 1 T; 0 U; 0 Other;
                                                                                                          2066 САААААААААААААААААААААААААААААА
                                                              Best Loca
Matches
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4 саадададададададададададададада 36
                          BP
                          AAN70278 standard; DNA; 32
                                               (revised)
(first entry)
                                               03-OCT-2002
26-MAY-1991
                                    AAN70278;
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Sequence of scissile link probe MRC068 (HL).

Hybridisation; probe; ss

Synthetic

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The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and NA2 are noncomplementary nucleic acid sequences; ---S--- a scissile linkage; n= 1 or 1,000, which is used for the detection of specific DNA or RNA sequences in a test soln. The scissile link probes may be PL or RNA sequences in a test soln. The scissile link probes may be PL support). The differential liability of DNA and RNA may be exploited in a betrerogenous system when the scissile linkage is an RNA may be exploited in a examples, counter probe molecules 9 through 16 were used to determine synthials hybridisation conditions. (Updated on 03-OCT-2002 to add missing
                                                                                                                                                                                                                                      Synthetic nucleic acid probes - comprising two nucleic acid sequences linked by a scissile linkage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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100.0%; Pred. No. 0.027;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 32 BP; 0 A; 0 C; 0 G; 24 T; 8 U; 0 Other;
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                                                                                                                                                                           Robertson JG;
                                                                                                                                                                              Crosby W,
                                                                                                          85US-00805279
                                                                                                                                                                                                                                                                                                Example; p29; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 100.
Matches 32; Conservative
                                                                                                                                               (MEIO-) MEIOGENICS INC
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                                                                                                                                                                                Bender R,
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